

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 20, 2004, 16:27:40 ; Search time 94 Seconds

(without alignments)
1175.233 Million cell updates/sec

Title: US-09-783-931-65

Perfect score: 1160

Sequence: 1 GFTWPGTFLIIEALHTDSP.....CNQDLNYCTHKKCKNGATC 192

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 segs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1160	100.0	723	1 DLI1_HUMAN	O00548 homo sapien
2	1138	98.1	728	2 Q90656	Q90656 gallus gall
3	1125	97.0	714	1 DLI1_RAT	P97677 rattus norv
4	1122	96.7	722	1 DLI1_MOUSE	Q61483 mus musculu
5	1122	96.7	722	2 Q6PFV7	Q6PFV7 mus musculu
6	1122	96.7	722	2 AAH57400	Aah57400 mus muscu
7	1122	96.7	722	2 AAR30869	Aar30869 mus muscu
8	1122	96.7	722	2 AAH65063	Aah65063 mus muscu
9	1074	92.8	721	2 Q91902	Q91902 xenopus lae
10	1074	92.6	726	2 Q8AW87	Q8AW87 cynops pyrr
11	1059	91.3	717	2 P87357	P87357 brachydantio
12	1059	91.3	720	2 Q8UWJ4	Q8UWJ4 brachydantio
13	1054	90.9	772	2 Q6DI48	Q6DI48 brachydantio
14	1054	90.9	802	2 Q57462	Q57462 brachydantio
15	835.5	72.0	642	2 P79941	P79941 xenopus lae
16	835.5	72.0	642	2 Q7ZXT4	Q7ZXT4 xenopus lae
17	794	68.4	615	2 Q57409	Q57409 brachydantio
18	742.5	66.8	664	2 Q9IAT6	Q9IAT6 brachydantio
19	742.5	64.0	684	2 Q8I498	Q8I498 cuplenius
20	709.5	61.2	685	1 DLI4_HUMAN	Q9N961 homo sapien
21	685.5	59.1	438	2 Q8I497	Q8I497 cuplenius
22	680.5	58.7	686	1 DLI4_MOUSE	Q9J171 mus musculu
23	680.5	58.7	686	2 Q9DBU9	Q9DBU9 mus musculu
24	676	58.3	650	2 Q7Q0M5	Q7Q0M5 anopheles g
25	659.5	56.9	833	1 DL_DROME	P10041 drosophila
26	659.5	56.9	833	2 Q6T4M9	Q6T4M9 drosophila
27	659.5	56.9	833	2 Q6T4N0	Q6T4N0 drosophila
28	659.5	56.9	833	2 Q6T4N1	Q6T4N1 drosophila
29	659.5	56.9	833	2 Q6T4N2	Q6T4N2 drosophila
30	659.5	56.9	833	2 Q6T4N3	Q6T4N3 drosophila
31	659.5	56.9	833	2 Q6T4N4	Q6T4N4 drosophila

32	659.5	56.9	833	2 Q6T4N6	Q6T4N6 drosophila
33	659.5	56.9	833	2 AAO25024	AAO25024 drosophila
34	659.5	56.9	833	2 AAR21453	AAR21453 drosophila
35	659.5	56.9	833	2 AAR21454	AAR21454 drosophila
36	659.5	56.9	833	2 AAR21455	AAR21455 drosophila
37	659.5	56.9	833	2 AAR21456	AAR21456 drosophila
38	659.5	56.9	833	2 AAR21457	AAR21457 drosophila
39	659.5	56.9	833	2 AAR21458	AAR21458 drosophila
40	659.5	56.9	833	2 AAR21459	AAR21459 drosophila
41	659.5	56.9	833	2 AAR21460	AAR21460 drosophila
42	659.5	56.9	833	2 AAR21461	AAR21461 drosophila
43	659.5	56.9	833	2 AAR21462	AAR21462 drosophila
44	659.5	56.9	833	2 AAR21463	AAR21463 drosophila
45	659.5	56.9	833	2 AAR21464	AAR21464 drosophila

ALIGNMENTS

RESULT 1	DLI1_HUMAN	STANDARD:	PRT;	723 AA.
ID	DLI1_HUMAN			
AC	O00548; Q9NU41; Q9UTV2;			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Delta-like protein 1 precursor (Drosophila Delta homolog 1) (Delta1)			
DE	(H-Delta-1) (UNQ146/PRO172).			
GN	Name=DLI1;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99180765; Pubmed=10079256;			
RA	Gray G.E., Mann R.S., Mitsiadis B., Henrique D., Carcangiu M.-L.,			
RA	Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.;			
RT	"Human ligands of the Notch receptor."			
RL	Am. J. Pathol. 154:785-794(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Han W., Ye Q., Moore M.A.S.;			
RT	"A soluble form of human delta-like-1 inhibits differentiation of			
RT	hematopoietic progenitor cells."			
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Oda T., Chandrasekharappa S.C.;			
RT	"Human Delta 1 gene sequence."			
RL	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=22887296; Pubmed=12975309; DOI=10.1101/gr.1293003;			
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,			
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,			
RA	Baton D., Foster J., Grimaldi C., Gu Q., Hass P.B., Heldens S.,			
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,			
RA	Lewis L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld J.,			
RA	Seshagiri S., Stimmens L., Singh J., Smith V., Stinson J., Vagts A.,			
RA	Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.-H., Yansura D.,			
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,			
RA	Godowski P.;			
RT	"The secreted protein discovery initiative (SPDI), a large-scale			
RT	effort to identify novel human secreted and transmembrane proteins: a			
RT	bioinformatics assessment."			
RL	Genome Res. 13:2265-2270(2003).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RA	Almeida J.;			
RL	Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.			
RN	[6]			
RP	FUNCTION.			

RA MEDLINE=21464863; PubMed=11581320;
RA Jaleco A.C., Neves H., Hoolberg E., Gameiro P., Clode N., Haury M.,
RA Henrique D., Parreira L.;
RT "Differential effects of Notch ligands Delta-1 and Jagged-1 in human
RT lymphoid differentiation.";
RL J. Exp. Med. 194:991-1001(2001).
CC -1- FUNCTION: Acts as a ligand for Notch receptors. Blocks the
CC differentiation of progenitor cells into the B-cell lineage while
CC promoting the emergence of a population of cells with the
CC characteristics of a T-cell/NK-cell precursor.
CC -1- SUBUNIT: Interacts with Notch receptors.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in heart and pancreas, with lower
CC expression in brain and muscle and almost no expression in
CC placenta, lung, liver, and kidney.
CC -1- SIMILARITY: Contains 1 DSL domain.
CC -1- SIMILARITY: Contains 8 EGF-like domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC -----
CC EMBL; AF003522; AAB61286.1; -.
CC EMBL; AF196571; AAF05834.1; -.
CC EMBL; AF222310; AAG09716.1; -.
CC EMBL; AY358892; AAQ89251.1; -.
CC EMBL; AL078605; CAB89569.1; -.
CC HSSP; P00740; 1EDM.
CC Genew; HGNC:2908; DLL1.
CC MIM; 606582; -.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0005887; C:integral to plasma membrane; NAS.
DR GO; GO:0005112; F:Notch binding; IPI.
DR GO; GO:0030154; P:cell differentiation; TAS.
DR GO; GO:0001709; P:cell fate determination; NAS.
DR GO; GO:0001701; P:embryonic development (sensu Mammalia); ISS.
DR GO; GO:000912; P:hair cell fate commitment; ISS.
DR GO; GO:0030097; P:hemopoiesis; NAS.
DR GO; GO:0042472; P:inner ear morphogenesis; ISS.
DR GO; GO:0007399; P:neurogenesis; ISS.
DR GO; GO:0007219; P:Notch signaling pathway; NAS.
DR GO; GO:0042475; P:odontogenesis (sensu Vertebrata); ISS.
DR GO; GO:0030155; P:regulation of cell adhesion; TAS.
DR InterPro; IPR000152; Asx_hydroxyl_5.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_IIlike.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 6.
DR PRINTS; PR00010; EGFBLDOD.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00179; EGF_CA; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; 8.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS50026; EGF_3; 7.
DR PROSITE; PS01187; EGF_CA; 1.
KW Developmental protein; Differentiation; EGF-like domain; Glycoprotein;
KW Repeat; Signal; Transmembrane.
FT SIGNAL 1 17 Potential.
FT CHAIN 18 723 Delta-like protein 1.
FT DOMAIN 18 545 Extracellular (Potential).
FT TRANSMEM 546 568 Potential.
FT DOMAIN 569 723 Cytoplasmic (Potential).
FT DOMAIN 159 221 DSL.
FT DOMAIN 226 254 EGF-like 1.
FT DOMAIN 257 285 EGF-like 2.

FT DOMAIN 292 325 EGF-like 3.
FT DOMAIN 332 363 EGF-like 4, calcium-binding (Potential).
FT DOMAIN 370 402 EGF-like 5.
FT DOMAIN 409 440 EGF-like 6.
FT DOMAIN 447 478 EGF-like 7, calcium-binding (Potential).
FT DOMAIN 485 516 EGF-like 8.
FT DISULFID 226 237 By similarity.
FT DISULFID 230 243 By similarity.
FT DISULFID 245 254 By similarity.
FT DISULFID 257 268 By similarity.
FT DISULFID 263 274 By similarity.
FT DISULFID 276 285 By similarity.
FT DISULFID 292 304 By similarity.
FT DISULFID 298 314 By similarity.
FT DISULFID 316 325 By similarity.
FT DISULFID 332 343 By similarity.
FT DISULFID 337 352 By similarity.
FT DISULFID 354 363 By similarity.
FT DISULFID 370 381 By similarity.
FT DISULFID 375 391 By similarity.
FT DISULFID 393 402 By similarity.
FT DISULFID 409 420 By similarity.
FT DISULFID 414 429 By similarity.
FT DISULFID 431 440 By similarity.
FT DISULFID 447 467 By similarity.
FT DISULFID 469 478 By similarity.
FT DISULFID 485 496 By similarity.
FT DISULFID 490 505 By similarity.
FT DISULFID 507 516 By similarity.
FT CARBOHYD 477 477 N-linked (GlcNAc...) (Potential).
FT CONFLICT 498 498 E -> Q (in Ref. 2).
FT CONFLICT 502 502 G -> R (in Ref. 4 and 5).
FT CONFLICT 510 510 G -> S (in Ref. 2).
SQ SEQUENCE 723 AA; 77956 MW; B4EC455FFA32A12B CRC64;

Query Match 100.0%; Score 1160; DB 1; Length 723;
Best Local Similarity 100.0%; Pred. No. 3.5e-88;
Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTWPGTFLIIEALHTDSPDDLATENPERLISRLATQRLHVTGEBSQDLHSSGRTDLK 60
Db 113 GFTWPGTFLIIEALHTDSPDDLATENPERLISRLATQRLHVTGEBSQDLHSSGRTDLK 172
QY 61 YSYRFVCDHEHYEGGCVFCRPRDAFGHFTGGERGEKVCNPGWKGPYCTEPICLPGCDE 120
Db 173 YSYRFVCDHEHYEGGCVFCRPRDAFGHFTGGERGEKVCNPGWKGPYCTEPICLPGCDE 232
QY 121 QHGFCDKPGECKCRVGNQGRYCDCEIRYPGCLHGTCCQPPWQCNCQEGWGGLFCNDLNYC 180
Db 233 QHGFCDKPGECKCRVGNQGRYCDCEIRYPGCLHGTCCQPPWQCNCQEGWGGLFCNDLNYC 292
QY 181 THHKPCKNKATC 192
Db 293 THHKPCKNKATC 304

RESULT 2
ID Q90656 PRELIMINARY; PRT; 728 AA.
AC Q90656;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE C-Delta-1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spinal cord;
RX MEDLINE=95319507; PubMed=7596411;

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OM protein - protein search, using sw model

Run on: November 20, 2004, 16:28:50 / Search time 22 seconds

(without alignments)
839.710 Million cell updates/sec

Title: US-09-783-931-65

Perfect score: 1160

Sequence: 1 GFTWPGTFLIIEALHTDSP.....CNQDLNYCTHHKPKNGATC 192

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR_79: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1138	98.1	728	2 150719	C-Delta-1 - chicken
2	1122	96.7	722	2 148324	DELTA-like 1 - mou
3	709.5	61.2	685	2 JC7570	Delta-4 protein -
4	680.5	58.7	686	2 JC7569	Delta-4 protein -
5	659.5	56.9	832	2 A31246	neurogenic protein
6	659.5	56.9	833	2 S19087	gene Delta protein
7	659.5	56.9	880	2 S00670	neurogenic repetit
8	587	50.6	1220	2 A56136	jagged protein pre
9	533	45.9	1408	2 S16148	gene serrate prote
10	299.5	25.8	513	2 D88991	protein apx-1 (imp
11	288.5	24.9	385	2 S53718	homeotic protein d
12	280.5	24.2	385	2 A54785	preadipocyte facto
13	272.5	23.5	308	2 UC7125	epidermal growth f
14	272.5	23.5	383	2 S53716	delta-like homeoti
15	224.5	19.4	259	2 T21011	hypothetical prote
16	223.5	19.3	782	2 A61625	tenascin-like prot
17	211.5	18.2	3191	2 T22945	hypothetical prote
18	210.5	18.1	379	2 A59180	wnt inhibitory fac
19	207	17.8	2471	2 A49128	cell-face determin
20	205	17.7	1203	2 A49175	Notch B protein -
21	203.5	17.5	1111	2 T26972	hypothetical prote
22	197	17.0	2406	2 A54148	od3 protein - frut
23	197	17.0	2515	2 S47008	tenascin-like prot
24	196	16.9	2318	2 S45306	notch 3 protein -
25	195	16.8	2321	2 S78549	notch3 protein - h
26	193	16.6	2019	1 JQ1322	tenascin precursor
27	193	16.6	2524	2 A35844	Xotch protein - Af
28	190.5	16.4	1429	2 S06434	homeotic protein 1
29	188	16.2	1295	2 A32901	glt1 protein precu

30	187.5	16.2	2825	2 T14271	Doc4 protein, stre
31	185.5	16.0	2555	2 A40043	notch protein homo
32	185	15.9	1746	1 S19694	tenascin precursor
33	184.5	15.9	378	2 B59180	wnt inhibitory fac
34	184.5	15.9	1964	2 T09059	notch4 - mouse
35	184	15.9	2531	2 A46019	notch-1 protein -
36	183	15.8	2437	2 S42612	transmembrane prot
37	182.5	15.7	2918	2 A54105	fibritillin-2 precu
38	181.5	15.6	1574	2 T13954	MEGF6 protein - ra
39	181.5	15.6	2531	2 S18188	notch protein homo
40	180.5	15.6	2139	2 A35672	crumbs protein - f
41	180.5	15.6	2703	1 A24420	notch protein - fr
42	180	15.5	473	2 A56175	adhesive plaque pr
43	179.5	15.5	2352	2 T30201	Notch homolog pr
44	178	15.3	2201	2 A32160	tenascin-C - human
45	177.5	15.3	861	2 A48825	Notch homolog Motc

ALIGNMENTS

RESULT 1

150719

C-Delta-1 - chicken

C/Species: Gallus gallus (chicken)

C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004

C/Accession: 150719

R/Henrique, D.; Adam, J.; Myat, A.; Chitnis, A.; Lewis, J.; Ish-Horowitz, D.

Nature 375, 787-790, 1995

A/Title: Expression of a Delta homologue in prospective neurons in the chick.

A/Reference number: 150719, MUID:95319507, PMID:7596411

A/Accession: 150719

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-728 <HEN>

A/Cross-references: UNIPROT:Q90656; EMBL:U26590; NID:9882411, PIDN:AAC59689.1, PID:9882

C/Superfamily: delta-4 protein; EGF homology

F/299-332/Domain: EGF homology <EGX1>

F/339-370/Domain: EGF homology <EGF1>

F/416-447/Domain: EGF homology <EGX2>

F/454-485/Domain: EGF homology <EGF>

F/492-523/Domain: EGF homology <EGF3>

Query Match 98.1%; Score 1138; DB 2; Length 728;
Best Local Similarity 97.9%; Pred. No. 6.1e-79;
Matches 188; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY	1	GFTWPGTFLIIEALHTDSPDDLATENPERLISRLATQRLTVGEWSQDLHSGRTDLK	60
DB	120	GFTWPGTFLIIEALHTDSPDDLTTENPERLISRLATQRLTVGEWSQDLHSGRTDLK	179
QY	61	YSYRFVCDENHYEGGCVFCRPRDDAFGHFTGGERGEKVCNPGMKGPYCTEPICLPGCDE	120
DB	180	YSYRFVCDENHYEGGCVFCRPRDDRFHFTGGERGEKVCNPGMKGPYCTEPICLPGCDE	239
QY	121	QHGFCDKPGBECKRGVWGRCYDCRCIRYPGCLHGTCCQPMQCNCQEGWGGLFCNQDLNYC	180
DB	240	QHGFCDKPGBECKRGVWGRCYDCRCIRYPGCLHGTCCQPMQCNCQEGWGGLFCNQDLNYC	299
QY	181	THHKPKNGATC 192	
DB	300	THHKPKNGATC 311	

RESULT 2

148324

DELTA-like 1 - mouse

C/Species: Mus musculus (house mouse)

C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C/Accession: 148324

R/Bettenhausen, B.; de Angelis, M.H.; Simon, D.; Guenet, J.L.; Gossler, A.

Development 121, 2407-2418, 1995

A/Title: Transient and restricted expression during mouse embryogenesis of Dll1, a murin

A/Reference number: I48324, MUID:95401858, PMID:7671806
A/Accession: I48324
A/Status: preliminary/ translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-722 <RBS>
A/Cross-references: UNIPROT:Q61483; EMBL:X80903, NID:g806569; PIDN:CAA56865.1; PID:g8065
C/Genetics:
A/Gene: D11
C/Superfamily: delta-4 protein, EGF homology
F,331-362/Domain: EGF homology <EGF2>
F,446-477/Domain: EGF homology <EGF>
F,484-515/Domain: EGF homology <EGF1>

Query Match 96.7%; Score 1122; DB 2; Length 722;
Best Local Similarity 94.8%; Pred. No. 9.8e-78;
Matches 182; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTWPGTSLIIEALHTDSPDDLATENPERLISRLATQRLTVGEWESQDLHSSGRTDLK 60
DB 112 GFTWPGTSLIIEALHTDSPDDLATENPERLISRLATQRLTVGEWESQDLHSSGRTDLR 171
QY 61 YSVRFVCDHEHYEGGCVFCRPRDAFGHFTGGERGEKVCNPGWKGPYCTBPICLPGCD 120
DB 172 YSVRFVCDHEHYEGGCVFCRPRDAFGHFTGGERGEKVCNPGWKGPYCTBPICLPGCD 231
QY 121 QHGFCDKPECKCRVWGGRYCDICTIRYPGCLHGTCCQPMQCNQOEGWGLFCNQDLNYC 180
DB 232 QHGFCDKPECKCRVWGGRYCDICTIRYPGCLHGTCCQPMQCNQOEGWGLFCNQDLNYC 291
QY 181 THHKPCXNGATC 192
DB 292 THHKPCXNGATC 303

RESULT 3

JC7570
Delta-4 protein - human
C/Species: Homo sapiens (man)
C/Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C/Accession: JC7570
R/Yoneya, T.; Tahara, T.; Nagao, K.; Yamada, Y.; Yamamoto, T.; Osawa, M.; Miyatani, S.;
J. Biochem. 129, 27-34, 2001
A/Title: Molecular cloning of Delta-4, a new mouse and human notch ligand.
A/Reference number: JC7569, MUID: 21064937, PMID:11134954
A/Accession: JC7570
A/Molecule type: mRNA
A/Residues: 1-685 <YON>
A/Cross-references: UNIPROT:Q9NR61; DBJ:AB043894
C/Comment: This protein, a member of the Notch family of proteins, is a transmembrane re
ates the Notch signaling, the growth or differentiation of vascular endothelial cells.
C/Genetics:
A/Gene: delta-4
C/Superfamily: delta-4 protein; EGF homology
C/Keywords: transmembrane protein

Query Match 61.2%; Score 709.5; DB 2; Length 685;
Best Local Similarity 61.1%; Pred. No. 1.7e-46;
Matches 118; Conservative 19; Mismatches 53; Indels 3; Gaps 2;

QY 2 FTWPGTSLIIEALHTDSPDDLATENPERLISRLATQRLTVGEWESQDLHSSGRTDL 59
DB 109 FTWPGTSLIIEALHTDSPDDLATENPERLISRLATQRLTVGEWESQDLHSSGRTDL 167
QY 60 KYSYRFVCDHEHYEGGCVFCRPRDAFGHFTGGERGEKVCNPGWKGPYCTBPICLPGCD 119
DB 168 KYSYRFVCDHEHYEGGCVFCRPRDAFGHFTGGERGEKVCNPGWKGPYCTBPICLPGCD 227
QY 120 EOHGFCDKPECKCRVWGGRYCDICTIRYPGCLHGTCCQPMQCNQOEGWGLFCNQDLNY 179
DB 228 EOHGFCDKPECKCRVWGGRYCDICTIRYPGCLHGTCCQPMQCNQOEGWGLFCNQDLNY 287
QY 180 CTHHKPCXNGATC 192
DB 292 CTHHKPCXNGATC 303

DB 288 CTHHKPCXNGATC 300

RESULT 4

JC7569
Delta-4 protein - mouse
C/Species: Mus musculus (house mouse)
C/Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C/Accession: JC7569
R/Yoneya, T.; Tahara, T.; Nagao, K.; Yamada, Y.; Yamamoto, T.; Osawa, M.; Miyatani, S.;
J. Biochem. 129, 27-34, 2001
A/Title: Molecular cloning of Delta-4, a new mouse and human notch ligand.
A/Reference number: JC7569, MUID: 21064937, PMID:11134954
A/Accession: JC7569
A/Molecule type: mRNA
A/Residues: 1-686 <YON>
A/Cross-references: UNIPROT:Q9DBU9; DBJ:AB043893
C/Comment: This protein, a member of the Notch family of proteins, is a transmembrane r
ates the Notch signaling, the growth or differentiation of vascular endothelial cells.
C/Genetics:
A/Gene: delta-4
C/Superfamily: delta-4 protein; EGF homology

Query Match 58.7%; Score 680.5; DB 2; Length 686;
Best Local Similarity 59.6%; Pred. No. 2.6e-44;
Matches 115; Conservative 17; Mismatches 58; Indels 3; Gaps 2;

QY 2 FTWPGTSLIIEALHTDSPDDLATENP-ERLISRLATQRLTVGEWESQDLHSSGRTDL 59
DB 110 FTWPGTSLIIEALHTDSPDDLATENP-ERLISRLATQRLTVGEWESQDLHSSGRTDL 168
QY 60 KYSYRFVCDHEHYEGGCVFCRPRDAFGHFTGGERGEKVCNPGWKGPYCTBPICLPGCD 119
DB 169 KYSYRFVCDHEHYEGGCVFCRPRDAFGHFTGGERGEKVCNPGWKGPYCTBPICLPGCD 228
QY 120 EOHGFCDKPECKCRVWGGRYCDICTIRYPGCLHGTCCQPMQCNQOEGWGLFCNQDLNY 179
DB 229 EOHGFCDKPECKCRVWGGRYCDICTIRYPGCLHGTCCQPMQCNQOEGWGLFCNQDLNY 288
QY 180 CTHHKPCXNGATC 192
DB 289 CTHHKPCXNGATC 301

RESULT 5

A31246
neurogenic protein Delta precursor - fruit fly (Drosophila melanogaster)
C/Species: Drosophila melanogaster
C/Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 02-Aug-2002
C/Accession: A31246
R/Kopczynski, C.C.; Altou, A.K.; Fechtel, K.; Kooh, P.J.; Muskavitch, M.A.T.
Genes Dev. 2, 1723-1735, 1988
A/Title: Delta, a Drosophila neurogenic gene, is transcriptionally complex and encodes
A/Reference number: A31246; MUID:89196890; PMID:3149249
A/Accession: A31246
A/Molecule type: mRNA
A/Residues: 1-832 <KOP>
A/Cross-references: GB:Y00222
C/Genetics:
A/Gene: FlyBase:DL

A/Cross-references: FlyBase:FBgn000463
C/Superfamily: neurogenic protein delta; EGF homology
F,295-328/Domain: EGF homology <EGF1>
F,422-450/Domain: EGF homology <EGF2>
F,457-488/Domain: EGF homology <EGF3>
F,533-564/Domain: EGF homology <EGF3>

Query Match 56.9%; Score 659.5; DB 2; Length 832;
Best Local Similarity 56.0%; Pred. No. 1.2e-42;
Matches 107; Conservative 25; Mismatches 56; Indels 3; Gaps 2;

QY 2 FTWPGTSLIIEALHTDSPDDLATENPERLISRLATQRLTVGEWESQDLHSSGRTDLK 61
DB 292 FTWPGTSLIIEALHTDSPDDLATENPERLISRLATQRLTVGEWESQDLHSSGRTDLK 168

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 20, 2004, 16:36:05 ; Search time 69 Seconds

(without alignments)
985.399 Million cell updates/sec

Title: US-09-783-931-65

Perfect score: 1160

Sequence: 1 GFTWPGTFSLIIEALHTDSP.....CNQDLNYCTHKKCKNGATC 192

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
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- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1160	100.0	192	9	US-09-908-322-65	Sequence 65, Appl
2	1160	100.0	192	10	US-09-783-931-65	Sequence 65, Appl
3	1160	100.0	276	9	US-09-908-322-43	Sequence 43, Appl
4	1160	100.0	276	10	US-09-783-931-43	Sequence 43, Appl
5	1160	100.0	520	9	US-09-995-593A-3	Sequence 3, Appl1
6	1160	100.0	702	9	US-09-995-593A-4	Sequence 4, Appl1
7	1160	100.0	723	9	US-09-828-366-21	Sequence 21, Appl1
8	1160	100.0	723	9	US-09-995-593A-9	Sequence 9, Appl1
9	1160	100.0	723	14	US-10-028-072-346	Sequence 346, App
10	1160	100.0	723	14	US-10-140-808-346	Sequence 346, App
11	1160	100.0	723	14	US-10-121-049-346	Sequence 346, App
12	1160	100.0	723	14	US-10-123-504-346	Sequence 346, App
13	1160	100.0	723	14	US-10-140-470-346	Sequence 346, App

14	1160	100.0	723	14	US-10-175-746-346	Sequence 346, App
15	1160	100.0	723	14	US-10-176-918-346	Sequence 346, App
16	1160	100.0	723	14	US-10-176-921-346	Sequence 346, App
17	1160	100.0	723	14	US-10-137-865-346	Sequence 346, App
18	1160	100.0	723	14	US-10-140-474-346	Sequence 346, App
19	1160	100.0	723	14	US-10-142-431-346	Sequence 346, App
20	1160	100.0	723	14	US-10-143-114-346	Sequence 346, App
21	1160	100.0	723	14	US-10-140-002-346	Sequence 346, App
22	1160	100.0	723	14	US-10-142-419-346	Sequence 346, App
23	1160	100.0	723	14	US-10-241-476-27	Sequence 27, Appl1
24	1160	100.0	723	14	US-10-123-262-346	Sequence 346, App
25	1160	100.0	723	14	US-10-142-423-346	Sequence 346, App
26	1160	100.0	723	14	US-10-121-050-346	Sequence 346, App
27	1160	100.0	723	14	US-10-141-755-346	Sequence 346, App
28	1160	100.0	723	14	US-10-143-032-346	Sequence 346, App
29	1160	100.0	723	14	US-10-123-108-346	Sequence 346, App
30	1160	100.0	723	14	US-10-123-236-346	Sequence 346, App
31	1160	100.0	723	14	US-10-123-261-346	Sequence 346, App
32	1160	100.0	723	14	US-10-140-921-346	Sequence 346, App
33	1160	100.0	723	14	US-10-140-928-346	Sequence 346, App
34	1160	100.0	723	14	US-10-121-045-346	Sequence 346, App
35	1160	100.0	723	14	US-10-123-292-346	Sequence 346, App
36	1160	100.0	723	14	US-10-123-903-346	Sequence 346, App
37	1160	100.0	723	14	US-10-124-819-346	Sequence 346, App
38	1160	100.0	723	14	US-10-124-822-346	Sequence 346, App
39	1160	100.0	723	14	US-10-140-925-346	Sequence 346, App
40	1160	100.0	723	14	US-10-160-498-346	Sequence 346, App
41	1160	100.0	723	14	US-10-124-824-346	Sequence 346, App
42	1160	100.0	723	14	US-10-127-825A-346	Sequence 346, App
43	1160	100.0	723	14	US-10-127-829A-346	Sequence 346, App
44	1160	100.0	723	14	US-10-127-835A-346	Sequence 346, App
45	1160	100.0	723	14	US-10-127-839A-346	Sequence 346, App

ALIGNMENTS

RESULT 1
US-09-908-322-65
Sequence 65, Application US/09908322
Patent No. US20020107194A1

GENERAL INFORMATION:
APPLICANT: Ish-Horowicz, David
Henrique, Domingos Manuel Pinto
Lewie, Julian Hart
Artavanis-Tsakonas, Spyridon
Gray, Grace

TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF VERTEBRATE DELTA GENE AND METHODS BASED THEREON

NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/908,322
FILING DATE: 17-Jul-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997

ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-123

TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-908-322-65

Query Match 100.0%; Score 1160; DB 9; Length 192;
Best Local Similarity 100.0%; Pred. No. 2.2e-90;
Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTWPGTFSLLIBALHTDSPDDLATENPERLISRLATQRLTVGEWMSODLHSSGRTDLK 60
DB 1 GFTWPGTFSLLIBALHTDSPDDLATENPERLISRLATQRLTVGEWMSODLHSSGRTDLK 60
QY 61 YSYRFVCDENHYEGGCVFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDE 120
DB 61 YSYRFVCDENHYEGGCVFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDE 120
QY 121 QHGFCDKPECKCRVGMQGRYCDCEIRYPGCLHGTCCQPMQCNQCEGWSGLFCNQDLNYC 180
DB 121 QHGFCDKPECKCRVGMQGRYCDCEIRYPGCLHGTCCQPMQCNQCEGWSGLFCNQDLNYC 180
QY 181 THHKPCXNGATC 192
DB 181 THHKPCXNGATC 192

RESULT 2
US-09-783-931-65
Sequence 65, Application US/09783931
Publication No. US20030073620A1
GENERAL INFORMATION:
APPLICANT: Ish-Horowicz, David
Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon
Gray, Grace
TITLE OF INVENTION: ANTIBODIES TO VERTEBRATE DELTA PROTEINS
AND FRAGMENTS
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/783,931
FILING DATE: 15-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Antler, Adriane M.
REGISTRATION NUMBER: 32,605
REFERENCE/DOCKET NUMBER: 7326-122
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090

TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-783-931-65

Query Match 100.0%; Score 1160; DB 10; Length 192;
Best Local Similarity 100.0%; Pred. No. 2.2e-90;
Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTWPGTFSLLIBALHTDSPDDLATENPERLISRLATQRLTVGEWMSODLHSSGRTDLK 60
DB 1 GFTWPGTFSLLIBALHTDSPDDLATENPERLISRLATQRLTVGEWMSODLHSSGRTDLK 60
QY 61 YSYRFVCDENHYEGGCVFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDE 120
DB 61 YSYRFVCDENHYEGGCVFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDE 120
QY 121 QHGFCDKPECKCRVGMQGRYCDCEIRYPGCLHGTCCQPMQCNQCEGWSGLFCNQDLNYC 180
DB 121 QHGFCDKPECKCRVGMQGRYCDCEIRYPGCLHGTCCQPMQCNQCEGWSGLFCNQDLNYC 180
QY 181 THHKPCXNGATC 192
DB 181 THHKPCXNGATC 192

RESULT 3
US-09-908-322-43
Sequence 43, Application US/09908322
Patent No. US20020107194A1
GENERAL INFORMATION:
APPLICANT: Ish-Horowicz, David
Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon
Gray, Grace
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
VERTEBRATE DELTA GENE AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/908,322
FILING DATE: 17-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mierock, S Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE

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OM protein - protein search, using sw model

Run on: November 20, 2004, 15:47:05 / Search time 23 Seconds
(without alignments)
553.611 Million cell updates/sec

Title: US-09-783-931-65
Perfect score: 1160
Sequence: 1 GFTWPGTFLITLALHTDSP.....CNDLNYCTHHKPKNGATC 192

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1160	100.0	192	4	US-09-908-322-65 Sequence 65, Appl
3	1160	100.0	276	3	US-08-981-392-43 Sequence 43, Appl
4	1160	100.0	276	4	US-09-908-322-43 Sequence 43, Appl
5	1160	100.0	520	3	US-09-068-740A-3 Sequence 3, Appl
6	1160	100.0	702	3	US-09-068-740A-4 Sequence 4, Appl
7	1160	100.0	723	3	US-09-068-740A-9 Sequence 9, Appl
8	1160	100.0	723	4	US-09-423-753-27 Sequence 27, Appl
9	1160	100.0	723	4	US-10-140-002-346 Sequence 346, App
10	1153	99.4	723	4	US-09-641-612-6 Sequence 6, Appl
11	1138	98.1	728	4	US-08-981-392-2 Sequence 2, Appl
12	1138	98.1	728	4	US-09-908-322-2 Sequence 2, Appl
13	1138	98.1	729	3	US-08-872-855-8 Sequence 8, Appl
14	1119	96.5	722	3	US-08-981-392-12 Sequence 12, Appl
15	1119	96.5	722	4	US-09-908-322-12 Sequence 12, Appl
16	1110.5	95.7	713	3	US-08-872-855-5 Sequence 5, Appl
17	1107.5	95.5	720	3	US-08-872-855-4 Sequence 4, Appl
18	1077	92.8	721	3	US-08-981-392-5 Sequence 5, Appl
19	1077	92.8	721	4	US-09-908-322-5 Sequence 5, Appl
20	1072	92.4	721	4	US-08-872-855-7 Sequence 7, Appl
21	1059	91.3	717	3	US-08-872-855-9 Sequence 9, Appl
22	965	83.2	578	3	US-08-981-392-13 Sequence 13, Appl
23	965	83.2	578	4	US-09-908-322-13 Sequence 13, Appl
24	835.5	72.0	642	3	US-08-872-855-10 Sequence 10, Appl
25	709.5	61.2	500	4	US-09-423-753-2 Sequence 2, Appl
26	709.5	61.2	659	4	US-09-423-753-3 Sequence 3, Appl
27	709.5	61.2	685	3	US-08-872-855-2 Sequence 2, Appl

28	709.5	61.2	685	4	US-09-423-753-25 Sequence 25, Appl
29	709.5	61.2	685	4	US-09-641-612-7 Sequence 7, Appl
30	709.5	61.2	685	4	US-10-140-002-88 Sequence 88, Appl
31	659.5	56.9	830	3	US-08-872-855-11 Sequence 11, Appl
32	659.5	56.9	832	3	US-08-981-392-6 Sequence 6, Appl
33	659.5	56.9	832	4	US-09-908-322-6 Sequence 6, Appl
34	659.5	56.9	833	1	US-08-264-534-6 Sequence 2, Appl
35	659.5	56.9	833	1	US-08-083-590A-2 Sequence 2, Appl
36	659.5	56.9	833	1	US-08-465-500-6 Sequence 6, Appl
37	659.5	56.9	833	2	US-08-346-126-6 Sequence 6, Appl
38	659.5	56.9	833	2	US-08-346-128-6 Sequence 6, Appl
39	659.5	56.9	833	3	US-08-532-384-2 Sequence 2, Appl
40	659.5	56.9	833	3	US-08-893-828-6 Sequence 6, Appl
41	611	52.7	200	3	US-09-068-740A-2 Sequence 2, Appl
42	596	51.4	1193	2	US-08-400-159-10 Sequence 10, Appl
43	596	51.4	1193	3	US-08-611-729A-10 Sequence 10, Appl
44	596	51.4	1193	4	US-09-195-524-10 Sequence 10, Appl
45	591.5	51.0	1055	3	US-09-214-278-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-981-392-65
Sequence 65, Application US/08981392
Patent No. 6262025
GENERAL INFORMATION:
APPLICANT: Ish-Horowitz, David
APPLICANT: Henrique, Domingos Manuel Pinto
APPLICANT: Lewis, Julian Hart
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Gray, Grace
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,392
FILING DATE: 22-DEC-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Antler, Adriane M.
REGISTRATION NUMBER: 32,605
REFERENCE/DOCKET NUMBER: 7326-038
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-981-392-65

Query Match 100.0%; Score 1160; DB 3; Length 192;
Best Local Similarity 100.0%; Pred. No. 4.1e-92;
Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GFTWPGTFSLLIEALHTDSPDDLATENBERLISRLATORHLTVGBEWSQDLHSSGRTDLK	60
Db	1	GFTWPGTFSLLIEALHTDSPDDLATENBERLISRLATORHLTVGBEWSQDLHSSGRTDLK	60
QY	61	YSYRFVCDHEHYGEGCSVFCRPRDPAFGHFTGGERGSKVCNPGWKGPYCTBPICLPGBDE	120
Db	61	YSYRFVCDHEHYGEGCSVFCRPRDPAFGHFTGGERGSKVCNPGWKGPYCTBPICLPGBDE	120
QY	121	QHGFCDKPGECKCRVWGORYCDECIRYPGCLHGTCCQPMQCNCOEGWGGLFCNQDLNYC	180
Db	121	QHGFCDKPGECKCRVWGORYCDECIRYPGCLHGTCCQPMQCNCOEGWGGLFCNQDLNYC	180
QY	181	THHKPCXNGATC	192
Db	181	THHKPCXNGATC	192

RESULT 2

US-09-908-322-65
Sequence 65, Application US/09908322
Patent No. 6783956
GENERAL INFORMATION:
APPLICANT: Ish-Horowicz, David
Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon
Gray, Grace
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
VERTEBRATE DELTA GENE AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/908,322
FILING DATE: 17-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-908-322-65

```

Query Match      100.0%; Score 1160; DB 4; Length 192;
Best Local Similarity 100.0%; Pred. No. 4.1e-92;
Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 GFTWPGTFLIBALHTDSPDDLATENPERLISRRLATQRHLTVGEWSQDLHSSGRTDLK 60
|||||

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Db	1	GFTWPGTFSLLIEALHTDSDPDLATENPERLLISRLATQRLHVTVEEENSQDLHSSGRTDLK	60
QY	61	YSYRFVCDENHYGEGCSVFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDB	120
Db	61	YSYRFVCDENHYGEGCSVFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDB	120
QY	121	QHGFCDKPGECKCRVGMQGRYCDCEIRYPGLHGTCCQPMQCNCQEGMGGLFCNODLNYC	180
Db	121	QHGFCDKPGECKCRVGMQGRYCDCEIRYPGLHGTCCQPMQCNCQEGMGGLFCNODLNYC	180
QY	181	THHKPCXNGATC	192
Db	181	THHKPCXNGATC	192

RESULT 3

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US-08-981-392-43
/ Sequence 43, Application US/08981392
/ Patent No. 6262025
/
/ GENERAL INFORMATION:
/ APPLICANT: Ish-Horowitz, David
/ APPLICANT: Henrique, Domingos Manuel Pinto
/ APPLICANT: Lewis, Julian Hart
/ APPLICANT: Artavanis-Tsakonas, Spyridon
/ APPLICANT: Gray, Grace
/ TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
/ TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
/ NUMBER OF SEQUENCES: 94
/
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Penile & Edmonds LLP
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/
/ STATE: NY
/
/ COUNTRY: USA
/ ZIP: 10036/2711
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq Version 2.0
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/981,392
/ FILING DATE: 22-DEC-1997
/
/ CLASSIFICATION: 514
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Antler, Adriane M.
/ REGISTRATION NUMBER: 32,605
/ REFERENCE/DOCKET NUMBER: 7326-038
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 212-790-9090
/ TELEFAX: 212-869-8864
/
/ TELEX: 66141 PENNIB
/
/ INFORMATION FOR SEQ ID NO: 43:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 276 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: unknown
/ MOLECULE TYPE: peptide
/
US-08-981-392-43

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	Query Match	100.0%; Score 1160; DB 3;	Length 276;
	Best Local Similarity	100.0%;	Pred. No. 6.1e-92;
	Matches 192,	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
Qy	1 GFTWPGTFSLLIEALHTDSPDDLATENPRLISRLATQRHLTVGBEWSODLHSGRTDLK	60	
Dd	20 GFTWPGTFSLLIEALHTDSPDDLATENPRLISRATQRHLTVGBEWSODLHSSGRTDlk	79	
Qy	61 YSYRFVCDENHYEGGC SVFCRPRDAFGHFTCGERGEKYCNPMKGSPYCTBPICLPGCDE	120	
Dd	80 YSYRFVCDENHYEGGC SVFRCRPDDAFGHFTCGERGEKYCNPMKWGPYCTBPICLPgcDe	139	

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 20, 2004, 15:43:51 ; Search time 74 Seconds
(without alignments)
930.757 Million cell updates/sec

Title: US-09-783-931-65
Perfect score: 1160
Sequence: 1 GFTWPGTFLIIEALHTDSP.....CNQDLNCTHKKCKNGATC 192

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: geneseqp19808:*

2: geneseqp19908:*

3: geneseqp20008:*

4: geneseqp20018:*

5: geneseqp20028:*

6: geneseqp20038:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1160	100.0	192	2	AAW11728 H-Delta-1
2	1160	100.0	331	6	ABR61806 Human DLT
3	1160	100.0	331	7	ABR61735 Human DLT
4	1160	100.0	331	8	ADJ45785 Delta1 (D
5	1160	100.0	332	7	ABU63727 Notch 1lg
6	1160	100.0	332	8	ADJ45799 D1B3Cys p
7	1160	100.0	332	8	ADL73006 Human Not
8	1160	100.0	332	8	ADM75990 Human del
9	1160	100.0	369	6	ABR61807 Human DLT
10	1160	100.0	369	7	ABR61736 Human DLT
11	1160	100.0	369	8	ADJ45790 Delta1 (D
12	1160	100.0	369	8	ADL72998 Human Not
13	1160	100.0	484	6	ABR61808 Human DLT
14	1160	100.0	484	7	ABR61737 Human DLT
15	1160	100.0	484	8	ADJ45795 Delta1 (D
16	1160	100.0	484	8	ADL72986 Human Not
17	1160	100.0	512	2	AAW75494 Truncated
18	1160	100.0	520	2	AAW18348 Prolifera
19	1160	100.0	524	8	ADK67909 Human ext
20	1160	100.0	660	2	AAW11726 H-Delta-1
21	1160	100.0	702	2	AAW18349 Prolifera
22	1160	100.0	702	2	AAW75495 Truncated
23	1160	100.0	723	2	AAW18353 Prolifera
24	1160	100.0	723	2	AAW75492 Human del
25	1160	100.0	723	2	AAW94498 Human del

26	1160	100.0	723	3	AAW83227 PRO172 po
27	1160	100.0	723	3	AAB33422 Human PRO
28	1160	100.0	723	3	AAB24388 Human PRO
29	1160	100.0	723	3	AAW79032 Human del
30	1160	100.0	723	3	AAB00172 PRO172 po
31	1160	100.0	723	4	AAU12344 Human PRO
32	1160	100.0	723	4	AAB53064 Human ang
33	1160	100.0	723	6	ABO17788 Novel hum
34	1160	100.0	723	6	ABU81042 Human PRO
35	1160	100.0	723	6	ABP97824 Amino aci
36	1160	100.0	723	6	ABU66742 Human PRO
37	1160	100.0	723	6	ABU55879 Human not
38	1160	100.0	723	6	ABU59823 Novel sec
39	1160	100.0	723	6	ABO25013 Human sec
40	1160	100.0	723	6	ABP72566 Human Not
41	1160	100.0	723	6	ABU67018 Human sec
42	1160	100.0	723	6	ADA45865 Novel hum
43	1160	100.0	723	6	ADA76296 Human PRO
44	1160	100.0	723	6	ADA18946 Human PRO
45	1160	100.0	723	6	ADA18946 Human PRO

ALIGNMENTS

RESULT 1	AAW11728	standard; protein; 192 AA.
ID	AAW11728	
XX		
AC	AAW11728,	
XX		
DT	28-APR-1997	(first entry)
XX		
DE	H-Delta-1 polypeptide (aa 1-192).	
XX		
KW	H-Delta-1; cell proliferation; nervous system disorder;	
KW	tissue regeneration; Notch; cervix cancer; breast cancer; lung cancer;	
KW	colon cancer; melanoma; seminoma; neurogenesis; therapy.	
XX		
OS	Homo sapiens.	
XX		
PN	WO9701571-A1.	
XX		
PD	16-JAN-1997.	
XX		
PF	28-JUN-1996;	96WO-US011178.
XX		
PR	28-JUN-1995;	95US-0000589P.
XX		
PA	(IMCR) IMPERIAL CANCER RES TECHNOLOGY.	
PA	(UYTA) UNIV YALE.	
XX		
PI	Ish-Horowicz D, Henrique D, Lewis J, Artavanis-Tsakonas S;	
PI	Gray GB;	
XX		
DR	WPI; 1997-100159/09.	
XX		
PT	New vertebrate Delta protein, DNA and antibodies - for treating and	
PT	preventing cancer, nervous system disorders and for tissue regeneration.	
XX		
PS	Claim 84; Fig 14A; 135pp; English.	
XX		
CC	Human Delta-1 includes the polypeptide sequences given in AAW11728-38.	
CC	Amino acid residues 1-192 are given in AAW11728. The polypeptides were	
CC	identified from the translation products (see also AAW11725-27) of a H-	
CC	Delta-1 contig (AAT59454) derived from a foetal brain library. Errors in	
CC	the contig resulted in frameshifts, and the H-Delta-1 amino acid sequence	
CC	had to be deduced from the 3 translated sequences by homology to chick	
CC	and mouse Delta-1 (see also AAW11719-20). H-Delta-1 is a homologue of	
CC	Drosophila Delta, a protein that binds to Notch. H-Delta-1 polypeptides	
CC	can be used to treat disorders of cell fate or differentiation, such as	
CC	cancer, and nervous system disorders, or to promote tissue regeneration	
CC	and repair	

```
XX SO Sequence 192 AA;
Query Match 100.0%; Score 1160; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 2.3e-76;
Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTWPGTFSLLIHALHTDSPDDLATENPERLISRLATQRLHVTGGEWSQDLHSSGRTDLK 60
DB 1 GFTWPGTFSLLIHALHTDSPDDLATENPERLISRLATQRLHVTGGEWSQDLHSSGRTDLK 60
QY 61 YSYRFVCDHEHYEGGCSVFCRPRDDAFGHFTGGERGEKVCNPGWKGPYCTEPICLPGCDE 120
DB 61 YSYRFVCDHEHYEGGCSVFCRPRDDAFGHFTGGERGEKVCNPGWKGPYCTEPICLPGCDE 120
QY 121 QHGFCDKPGECKCRVGMGRYCDCEIRYPGCLHGTCCQPMQCNQEGMGGLFCNQDLNYC 180
DB 121 QHGFCDKPGECKCRVGMGRYCDCEIRYPGCLHGTCCQPMQCNQEGMGGLFCNQDLNYC 180
QY 181 THHKPCKNGATC 192
DB 181 THHKPCKNGATC 192

RESULT 2
ABR61806
ID ABR61806 standard; protein; 331 AA.
XX ABR61806;
XX 23-OCT-2003 (revised)
DT 03-SEP-2003 (first entry)
XX
DE Human DLL-1 EGF1-3-IgG4Fc fusion protein sequence.
XX
KW Notch signaling; notch ligand; immunostimulant; antimicrobial; EGF;
KW epidermal growth factor; medicament; vaccine; delta 1; DLL-1; IgG4Fc;
KW fusion protein.
XX
OS Homo sapiens.
OS Chimeric.
XX
PN WO2003041735-A2.
XX
PD 22-MAY-2003.
XX
PF 13-NOV-2002; 2002WO-GB005137.
XX
PR 14-NOV-2001; 2001GB-00027267.
PR 25-JUL-2002; 2002WO-GB003426.
PR 07-SEP-2002; 2002GB-00020849.
PR 10-SEP-2002; 2002GB-00020913.
PR 27-SEP-2002; 2002WO-GB004390.
XX
PA (LORA-) LORANTIS LTD.
XX
PI Bodmer MW, Briand ECP, Champion BR, Lennard AC, McKenzie GJ;
PI Ragno S, Tugal T, Young LL;
XX
DR WPI; 2003-449535/42.
XX
PT New product comprising a Notch signaling pathway inhibitor and a pathogen
PT antigen or antigenic determinant, useful for stimulating the immune
PT system to treat or prevent an infection, or for treating a chronic
PT pathogen infection.
XX
PS Example 21, Page 169-170; 256pp; English.
XX
CC The invention relates to a product comprising an inhibitor of the Notch
CC signaling pathway or a polynucleotide coding for such inhibitor; and a
CC pathogen antigen or antigenic determinant, or a polynucleotide coding for
CC such pathogen antigen or antigenic determinant, as a combined preparation
CC for simultaneous, contemporaneous, separate or sequential use for
```

```
CC modulating the immune system. The inhibitor of Notch signaling pathway is
CC useful in the manufacture of a medicament for use as a stimulant, but not
CC for reversing bacteria, infection, or tumor-induced immunosuppression, or
CC treating tumor. The inhibitor is also useful for stimulating the immune
CC system to treat or prevent an infection, in (enhancing) vaccination
CC against a pathogen, treating a chronic pathogen infection, and in
CC increasing the immune response of a subject to a vaccine antigen or
CC antigenic determinant. The binding agent that binds to a Notch ligand, an
CC antibody or its derivative that binds to a Notch receptor or Notch
CC ligand, or the polynucleotide encoding these, may also be used in the
CC manufacture of a medicament for use as a stimulant. The antibody or
CC antibody derivative may further be used in stimulating the immune system.
CC The present sequence represents a human delta 1 (DLL-1) EGF1-3-IgG4Fc
CC fusion protein. (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ Sequence 331 AA;
Query Match 100.0%; Score 1160; DB 6; Length 331;
Best Local Similarity 100.0%; Pred. No. 3.7e-76;
Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTWPGTFSLLIHALHTDSPDDLATENPERLISRLATQRLHVTGGEWSQDLHSSGRTDLK 60
DB 113 GFTWPGTFSLLIHALHTDSPDDLATENPERLISRLATQRLHVTGGEWSQDLHSSGRTDLK 172
QY 61 YSYRFVCDHEHYEGGCSVFCRPRDDAFGHFTGGERGEKVCNPGWKGPYCTEPICLPGCDE 120
DB 173 YSYRFVCDHEHYEGGCSVFCRPRDDAFGHFTGGERGEKVCNPGWKGPYCTEPICLPGCDE 232
QY 121 QHGFCDKPGECKCRVGMGRYCDCEIRYPGCLHGTCCQPMQCNQEGMGGLFCNQDLNYC 180
DB 233 QHGFCDKPGECKCRVGMGRYCDCEIRYPGCLHGTCCQPMQCNQEGMGGLFCNQDLNYC 292
QY 181 THHKPCKNGATC 192
DB 293 THHKPCKNGATC 304

RESULT 3
ABR61735
ID ABR61735 standard; protein; 331 AA.
XX ABR61735;
XX
DT 23-OCT-2003 (revised)
DT 02-SEP-2003 (first entry)
XX
DE Human DLL-1 EGF1-3-IgG4Fc fusion protein sequence.
XX
KW Notch signaling; cancer; notch ligand; epidermal growth factor; EGF;
KW cytosstatic; vaccine; human; delta 1; DLL-1; IgG4Fc; fusion protein.
XX
OS Homo sapiens.
OS Chimeric.
XX
PN WO2003042246-A2.
XX
PD 22-MAY-2003.
XX
PF 13-NOV-2002; 2002WO-GB005133.
XX
PR 14-NOV-2001; 2001GB-00027271.
PR 10-SEP-2002; 2002GB-00020913.
XX
PA (LORA-) LORANTIS LTD.
XX
PI Bodmer MW, Briand ECP, Champion BR, Lennard AC, McKenzie GJ;
PI Ragno S, Tugal T, Young LL;
XX
DR WPI; 2003-449560/42.
XX
PT New inhibitor of Notch signaling, useful for preventing or treating
PT cancer e.g. breast, liver, kidney or colon cancer.
```

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 20, 2004, 15:36:12 ; Search time 431 Seconds
(without alignments)
7597.670 Million cell updates/sec

Title: US-09-783-931-26_COPY_60_665
Perfect score: 606
Sequence: 1 GCTTCACCTGGCCGGGACAC.....GCCAGGGGAGCTACACTTG 606

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3627888 seqs, 2701811610 residues
Total number of hits satisfying chosen parameters: 7255776

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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2:	/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3:	/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4:	/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5:	/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6:	/cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7:	/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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11:	/cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12:	/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13:	/cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
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19:	/cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
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21:	/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	605	99.8	1981 9 US-09-908-322-26	Sequence 26, Appl
2	605	99.8	1981 10 US-09-783-931-26	Sequence 26, Appl
3	579.8	95.7	2183 17 US-10-644-548-9	Sequence 9, Appl
4	579.8	95.7	2663 9 US-09-995-593A-8	Sequence 8, Appl
5	579.8	95.7	2663 14 US-10-241-476-8	Sequence 8, Appl
6	579.8	95.7	2933 9 US-09-828-366-20	Sequence 20, Appl
7	579.8	95.7	2933 14 US-10-028-072-345	Sequence 345, App
8	579.8	95.7	2933 14 US-10-140-808-345	Sequence 345, App
9	579.8	95.7	2933 14 US-10-121-049-345	Sequence 345, App
10	579.8	95.7	2933 14 US-10-123-904-345	Sequence 345, App
11	579.8	95.7	2933 14 US-10-140-470-345	Sequence 345, App
12	579.8	95.7	2933 14 US-10-175-746-345	Sequence 345, App

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14	579.8	95.7	2933 14	US-10-176-921-345	Sequence 345, App
15	579.8	95.7	2933 14	US-10-137-865-345	Sequence 345, App
16	579.8	95.7	2933 14	US-10-474-345	Sequence 345, App
17	579.8	95.7	2933 14	US-10-142-431-345	Sequence 345, App
18	579.8	95.7	2933 14	US-10-143-114-345	Sequence 345, App
19	579.8	95.7	2933 14	US-10-140-002-345	Sequence 345, App
20	579.8	95.7	2933 14	US-10-142-419-345	Sequence 345, App
21	579.8	95.7	2933 14	US-10-123-262-345	Sequence 345, App
22	579.8	95.7	2933 14	US-10-142-423-345	Sequence 345, App
23	579.8	95.7	2933 14	US-10-121-050-345	Sequence 345, App
24	579.8	95.7	2933 14	US-10-141-755-345	Sequence 345, App
25	579.8	95.7	2933 14	US-10-143-032-345	Sequence 345, App
26	579.8	95.7	2933 14	US-10-123-108-345	Sequence 345, App
27	579.8	95.7	2933 14	US-10-123-236-345	Sequence 345, App
28	579.8	95.7	2933 14	US-10-123-261-345	Sequence 345, App
29	579.8	95.7	2933 14	US-10-140-921-345	Sequence 345, App
30	579.8	95.7	2933 14	US-10-140-928-345	Sequence 345, App
31	579.8	95.7	2933 14	US-10-121-045-345	Sequence 345, App
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33	579.8	95.7	2933 14	US-10-123-903-345	Sequence 345, App
34	579.8	95.7	2933 14	US-10-124-819-345	Sequence 345, App
35	579.8	95.7	2933 14	US-10-124-822-345	Sequence 345, App
36	579.8	95.7	2933 14	US-10-140-925-345	Sequence 345, App
37	579.8	95.7	2933 14	US-10-160-498-345	Sequence 345, App
38	579.8	95.7	2933 14	US-10-124-824-345	Sequence 345, App
39	579.8	95.7	2933 14	US-10-127-825A-345	Sequence 345, App
40	579.8	95.7	2933 14	US-10-127-829A-345	Sequence 345, App
41	579.8	95.7	2933 14	US-10-127-835A-345	Sequence 345, App
42	579.8	95.7	2933 14	US-10-127-839A-345	Sequence 345, App
43	579.8	95.7	2933 14	US-10-127-901A-345	Sequence 345, App
44	579.8	95.7	2933 14	US-10-128-693A-345	Sequence 345, App
45	579.8	95.7	2933 14	US-10-131-813A-345	Sequence 345, App

ALIGNMENTS

RESULT 1
US-09-908-322-26
Sequence 26, Application US/09908322
Patent No. US20020107194A1
GENERAL INFORMATION:
APPLICANT: Ish-Horowitz, David
Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon
Gray, Grace
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
VERTEBRATE DELTA GENE AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/908,322
FILING DATE: 17-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S Leslie
REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 7326-123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 1981 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-908-322-26

Query Match 99.8%; Score 605; DB 9; Length 1981;
Best Local Similarity 100.0%; Pred. No. 2.4e-179;
Matches 606; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-09-783-931-26
Sequence 26, Application US/09783931
Publication No. US20030073620A1
GENERAL INFORMATION:
APPLICANT: Ish-Horowitz, David
Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon

Gray, Grace
TITLE OF INVENTION: ANTIBODIES TO VERTEBRATE DELTA PROTEINS
AND FRAGMENTS
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESS: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/783,931
FILING DATE: 15-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Antler, Adriane M.
REGISTRATION NUMBER: 32,605
REFERENCE/DOCKET NUMBER: 7326-122
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 1981 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-783-931-26

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Best Local Similarity 100.0%; Pred. No. 2.4e-179;
Matches 606; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using SW model

Run on: November 20, 2004, 14:51:01 / Search time 72 Seconds

(without alignments)
5982.473 Million cell updates/sec

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/ptodata/1/lna/PCTUS_COMB.seq: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	605	99.8	1981	3	US-08-981-392-26 Sequence 26, Appl
2	605	99.8	1981	4	US-09-908-322-26 Sequence 26, Appl
3	579.8	95.7	2183	4	US-09-641-612-9 Sequence 9, Appl
4	579.8	95.7	2663	3	US-09-068-740A-8 Sequence 8, Appl
5	579.8	95.7	2663	4	US-09-423-753-8 Sequence 8, Appl
6	579.8	95.7	2933	4	US-10-140-002-345 Sequence 345, App
7	573	94.6	2899	3	US-08-981-392-24 Sequence 24, Appl
8	573	94.6	2899	4	US-09-908-322-24 Sequence 24, Appl
9	469.4	77.5	2508	3	US-08-981-392-1 Sequence 1, Appl
10	469.4	77.5	2508	4	US-09-908-322-1 Sequence 1, Appl
11	469.4	77.5	2883	3	US-08-981-392-3 Sequence 3, Appl
12	469.4	77.5	2883	4	US-09-908-322-3 Sequence 3, Appl
13	468.2	77.3	2692	3	US-08-981-392-11 Sequence 11, Appl
14	468.2	77.3	2692	4	US-09-908-322-11 Sequence 11, Appl
15	459.8	75.9	716	4	US-09-423-753-11 Sequence 11, Appl
16	457.4	75.5	2857	3	US-08-981-392-4 Sequence 4, Appl
17	457.4	75.5	2857	4	US-09-908-322-4 Sequence 4, Appl
18	220	36.3	2055	3	US-08-872-855-3 Sequence 3, Appl
19	220	36.3	2055	4	US-09-641-612-10 Sequence 10, Appl
20	220	36.3	2159	4	US-10-140-002-87 Sequence 87, Appl
21	220	36.3	2800	3	US-08-872-855-1 Sequence 1, Appl
22	220	36.3	3339	4	US-09-423-753-4 Sequence 4, Appl
23	178.8	29.5	4315	3	US-08-882-046-3 Sequence 3, Appl
24	178.8	29.5	4315	4	US-09-566-047-3 Sequence 3, Appl
25	178.6	29.5	2892	1	US-08-264-534-5 Sequence 5, Appl
26	178.6	29.5	2892	1	US-08-083-590A-1 Sequence 1, Appl
27	178.6	29.5	2892	1	US-08-465-500-5 Sequence 5, Appl

28	178.6	29.5	2892	2	US-08-346-126-5 Sequence 5, Appl
29	178.6	29.5	2892	2	US-08-346-128-5 Sequence 5, Appl
30	178.6	29.5	2892	3	US-08-532-384-1 Sequence 1, Appl
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33	177.2	29.2	3955	4	US-08-855-722-4 Sequence 4, Appl
34	177.2	29.2	4464	2	US-08-400-159-7 Sequence 7, Appl
35	177.2	29.2	4483	3	US-08-611-729A-7 Sequence 7, Appl
36	177.2	29.2	4483	4	US-09-195-524-7 Sequence 7, Appl
37	161.8	26.7	4208	3	US-09-214-278-6 Sequence 6, Appl
38	161.8	26.7	4208	3	US-09-068-740A-10 Sequence 10, Appl
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41	161.8	26.7	5590	4	US-09-566-047-1 Sequence 1, Appl
42	161.4	26.6	3201	4	US-09-579-536C-17 Sequence 17, Appl
43	161.4	26.6	3657	4	US-09-579-536C-2 Sequence 2, Appl
44	160.2	26.4	4855	4	US-09-917-254-34 Sequence 34, Appl
45	160.2	26.4	5458	4	US-09-199-865-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-981-392-26
Sequence 26, Application US/08981392
Patent No. 6262025
GENERAL INFORMATION:
APPLICANT: Ish-Horowicz, David
APPLICANT: Henrique, Domingos Manuel Pinto
APPLICANT: Lewis, Julian Hart
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Gray, Grace
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,392
FILING DATE: 22-DEC-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Antler, Adriane M.
REGISTRATION NUMBER: 32,605
REFERENCE/DOCKET NUMBER: 7326-038
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 1981 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-981-392-26

Query Match 99.8%, Score 605, DB 3, Length 1981,
Best Local Similarity 100.0%, Pred. No. 5.4e-170,
Matches 606, Conservative 0, Mismatches 0, Indels 0, Gaps 0,

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DB 660 CACTTG 665

RESULT 2

US-09-908-322-26
Sequence 26, Application US/09908322
Patent No. 6783956

GENERAL INFORMATION:

APPLICANT: Ish-Horowicz, David
Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon
Gray, Grace

TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
VERTEBRATE DELTA GENE AND METHODS BASED THEREON

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSES: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA

ZIP: 10036/2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/908,322

FILING DATE: 17-Jul-2001

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 1981 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-908-322-26

Query Match 99.8%; Score 605; DB 4; Length 1981;
Best Local Similarity 100.0%; Pred. No. 5.4e-170;
Matches 606; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 660 CACTTG 665

RESULT 3

US-09-641-612-9